

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 21, 2006, 03:52:16 ; Search time 352 Seconds
(without alignments) 139.107 Million cell updates/sec

Title: US-10-601-492-3

Perfect score: 21

Sequence: 1 cgvugagccgguuauucguu 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapept 1.0

Searched: 8023312 seqs, 1165852854 residues 13021146

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 15

Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_New.*

1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	85.7	19	10	US-11-101-244-613779
2	18	85.7	19	11	US-11-083-784-613779
3	15.2	72.4	25	7	US-10-934-048A-102729
4	14.8	70.5	25	12	US-11-121-849-216324
5	14.2	67.6	25	12	US-11-121-849-547830
6	14	66.7	25	7	US-10-933-982-75739
7	13.8	65.7	25	7	US-10-933-982-58238
8	13.8	65.7	25	12	US-11-121-849-547831
9	13.6	64.8	22	8	US-10-310-914A-236918
10	13.6	64.8	25	7	US-10-932-182A-111151
11	13.6	64.8	25	7	US-10-932-182A-194814
12	13.6	64.8	25	7	US-10-932-182A-111151
13	13.6	64.8	25	7	US-10-932-182A-194814
14	13.6	64.8	25	7	US-10-933-982-92677
15	13.4	63.8	19	10	US-11-101-244-1290409
16	13.4	63.8	19	10	US-11-101-244-1306752
17	13.4	63.8	19	11	US-11-083-784-1290409
18	13.4	63.8	19	11	US-11-083-784-1306752
19	13.4	63.8	24	12	US-11-069-908-5819
20	13.4	63.8	25	7	US-10-934-048A-78535

ALIGNMENTS

21 13.4 63.8 25 12 US-11-136-527-137380 Sequence 137380,
22 13.4 63.8 25 12 US-11-136-527-137384 Sequence 137384,
23 13.4 63.8 25 12 US-11-136-527-137385 Sequence 137385,
24 13.4 63.8 25 12 US-11-136-527-137387 Sequence 137387,
25 13.4 63.8 25 12 US-11-136-527-137388 Sequence 137388,
26 13.4 63.8 25 12 US-11-136-527-137393 Sequence 137393,
27 13.4 63.8 25 12 US-11-136-527-137396 Sequence 137396,
28 13.4 63.8 25 12 US-11-136-527-137398 Sequence 137398,
29 13.4 63.8 25 12 US-11-136-527-137398 Sequence 137398,
30 13.2 62.9 22 8 US-10-310-914A-214336 Sequence 214336,
31 13.2 62.9 23 8 US-10-310-914A-214325 Sequence 214325,
32 13.2 62.9 24 8 US-10-310-914A-214325 Sequence 214325,
33 13.2 62.9 25 7 US-10-932-182A-140982 Sequence 140982,
34 13.2 62.9 25 7 US-10-932-182A-140982 Sequence 140982,
35 13.2 62.9 25 7 US-10-933-982-82404 Sequence 82404, A
36 13.2 62.9 25 7 US-10-934-048A-25947 Sequence 25947, A
37 13.2 62.9 25 8 US-10-310-914A-116124 Sequence 116124,
38 13.2 62.9 25 12 US-11-121-849-49463 Sequence 49463, A
39 13.2 62.9 25 12 US-11-121-849-193840 Sequence 193840, A
40 13.2 62.9 25 12 US-11-121-849-309450 Sequence 309450,
41 13.2 62.9 25 12 US-11-121-849-178870 Sequence 178870,
42 13.2 62.9 28 8 US-10-310-914A-613834 Sequence 613834,
43 13 61.9 19 10 US-11-101-244-613834 Sequence 613834,
44 13 61.9 19 11 US-11-083-784-613834 Sequence 613834,
45 13 61.9 21 8 US-10-310-914A-385198 Sequence 385198,

RESULT 1
US-11-101-244-613779
; Sequence 613779, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 613779
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-613779

Query Match 85.7%; Score 18; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GUGAGCGGUUUCUGGU 21
Db 1 GUGAGCGGUUUCUGGU 18

RESULT 2
US-11-083-784-613779
; Sequence 613779, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia, Inc.
; APPLICANT: Khvorova, Anastasia

APPLICANT: Reynolds, Angela
 APPLICANT: Leeke, Devin
 APPLICANT: Marshall, William
 APPLICANT: Scaringe, Stephen
 TITLE OF INVENTION: Functional and Hyperfunctional sRNA
 FILE REFERENCE: 134950S
 CURRENT APPLICATION NUMBER: US/11/083,784
 CURRENT FILING DATE: 2005-03-18
 PRIOR APPLICATION NUMBER: US/10/714,333
 PRIOR FILING DATE: 2003-11-14
 PRIOR APPLICATION NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIOR APPLICATION NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO 613779
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-083-784-613779

Query Match	18;	Score	18;	DB	11;	Length	19;
Best Local Similarity	85.7%;	Pred. No.	1.7;				
Matches	18;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;

QY 4 GUGGACCGUUUAUCUGUU 21
|||||
Db 1 GUGGACCGUUUAUCUGUU 18

```

RESULT 3
US-10-934-048A-102729
: Sequence 102729, Application US/10934048A
: Publication NO. US20060051770A1
: GENERAL INFORMATION:
: APPLICANT: Tanya Makeev
: TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
: FILE REFERENCE: 3699
: CURRENT APPLICATION NUMBER: US/10/934,048A
: CURRENT FILING DATE: 2004-09-03
: NUMBER OF SEQ ID NOS: 120855
: SOFTWARE: Mclarrarray Probe Sequence Listing Generator V 1.1.1
: SEQ ID NO 102729
: LENGTH: 25
: TYPE: DNA
: ORGANISM: S. pombe
: US-10-934-048A-102729

```

Query Match	72.4%	Score 15.2	DB 7	length 25
Best Local Similarity	50.0%	Pred. No. 69		
Matches	10	Conservative	7	Mismatches 3
				Indels 0
				Gaps 0
Qy	2	cgucgacccguuauucgu	21	
	:			:
Db	2	ggtgcgaagcgtctatctat	21	

```

RESULT 4
US-11-121-849-216324
: Sequence 216324, Application US/11121849
: Publication NO. US20050272080A1
: GENERAL INFORMATION:
: APPLICANT: John Palma
: TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
: TITLE OF INVENTION: Microarrays
: FILE REFERENCE: 3684.1
: CURRENT APPLICATION NUMBER: US/11/121,849
: CURRENT FILING DATE: 2005-05-03
: PRIOR APPLICATION NUMBER: 60/567,949
: PRIOR FILING DATE: 2004-05-03
: NUMBER OF SEQ ID NOS: 673904
: SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

```

```

; SEQ ID NO 216324
;
; LENGTH: 25
;
; TYPE: DNA
;
; ORGANISM: Homo sapien
US-11-121-849-216324

```

Query Match	70.5%;	Score 14.8;	DB 12;	length 25;
Best Local Similarity	44.4%;	Pred. No. 1.2e+02;		
Matches	8;	Conservative	2;	Indels 0;
		Mismatches	2;	Gaps 0;

Dy 3 UGUGACCGUUUAUCUGU 20
 :::||||| :::: :
Db 5 TGTGCACCTTTATATGT 22

```

RESULT 5
US-11-121-849-547830/c
; Sequence 547830, Application US/11121849
; Publication No. US20050272080A1
;
GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 547830
;
LENGTH: 25
;
TYPE: DNA
;
ORGANISM: Homo sapien
;
US-11-121-849-547830

```

Query Match	67.6%	Score 14.2	DB 12	Length 25
Best Local Similarity	47.4%	Pred. No. 2.5e+02		
Matches 9	Conservative 7	Mismatches 3	Indels 0	Gaps 0

Oy		2	GUGUGACCGUUUAUUCUGU	20
	:: :: :			
D _b		23	GGTGGACTGTTAACTCT	5

RESULT 6
US-10-933-982-75739/c
; Sequence 75739, Application US/10933982
; Publication No. US20060051769A1

```

1  APPLICANT: Barts, Jennifer
2  TITLE OF INVENTION: Methods of Genetic Analysis of E. coli
3  FILE REFERENCE: 3700
4  CURRENT APPLICATION NUMBER: US/10/933,982
5  CURRENT FILING DATE: 2004-09-03
6  NUMBER OF SEQ ID NOS: 224976
7  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
8  SEQ ID NO 75739

```

; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: E. coli
 ; US-10-933-982-75739

```

Query Match      66.7%;  Score 14;  DB 7;  Length 25;
Best Local Similarity 50.0%;  Pred. NO. 3.3e+02;
Matches 7;  Conservative 7;  Mismatches 0;  Indels 0;  Gaps 0;

```

ay	8	ACCGUUUAVUCUGUU	21
		:: :: ::	
Db	25	ACCGTTATCTGTT	12

RESULT 7

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OM nucleic - nucleic search, using sw model

Run on: March 21, 2006, 03:25:27 ; Search time 579 Seconds
(without alignments)
241.725 Million cell updates/sec

Title: US-10-601-492-3

Perfect score: 21
Sequence: 1 cgugugagccgguuauucguu 21

Scoring table: IDENTITY NUC
Gapop 10-0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 3150182

Minimum DB seq length: 15
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	13	ADRI6250 Human Pab
2	19	90.5	21	13	ADRI6251 Human Pab
3	14.4	68.6	25	9	ACI17033 Human mic
4	14.2	67.6	25	9	ACK23852 Human mic
5	14.2	67.6	25	9	ACK23853 Human mic
6	14.2	67.6	26	4	AAH39289 SNP spect
7	13.8	65.7	23	14	AEBA22600 Urokinase
8	13.8	65.7	25	14	ADK69384 Pig Lep1
9	13.6	64.8	25	9	ACI693120 Human mic
10	13.4	63.8	20	6	ABO93101 T. tausch
11	13.4	63.8	25	9	ACI45565 Human mic
12	13.2	62.9	20	12	ADQ13747 DMD regio
13	13.2	62.9	25	9	ACI43660 Human mic
14	13.2	62.9	30	2	AAO85735 Rat 1 PCR
15	13	61.9	25	6	ABX14218 PCR prime
16	13	61.9	25	9	ACI96769 Human mic
17	13	61.9	26	5	AAI71940 Primer #4
18	13	61.9	26	6	ABX14214 PCR prime
19	13	61.9	28	5	AAI71943 Primer #6

20	13	61.9	30	3	AAA14417	AAA14417 Cornu con
C 21	12.8	61.0	24	6	ABQ03851	ABQ03851 Oligonuc1
C 22	12.8	61.0	25	9	ACK25229	ACK25229 Human mic
C 23	12.8	61.0	25	9	ACI27865	ACI27865 Human mic
24	12.8	61.0	25	9	ACK03756	ACK03756 Human mic
25	12.8	61.0	25	9	ACI17032	ACI17032 Human mic
26	12.8	61.0	25	11	ADM79618	ADM79618 Group B S
27	12.8	61.0	25	11	ADM79681	ADM79681 Group B S
28	12.8	61.0	30	6	ABK91929	ABK91929 Mouse CDC
29	12.6	60.0	20	12	ADL15507	ADL15507 PCR prime
C 30	12.6	60.0	20	13	ADT08168	ADT08168 CD11b gen
C 31	12.6	60.0	22	2	AAQ21659	AAQ21659 MMS compl
C 32	12.6	60.0	22	4	AAE92254	AAE92254 Human IGE
33	12.6	60.0	22	4	ADB81044	ADB81044 LINE felt
34	12.6	60.0	24	4	AAE92266	AAE92266 Human IGE
35	12.6	60.0	25	9	ACK17982	ACK17982 Human mic
C 36	12.6	60.0	25	9	ACI99227	ACI99227 Human mic
C 37	12.6	60.0	25	14	ADZ87090	ADZ87090 Human KCN
38	12.6	60.0	26	10	ADF66893	ADF66893 PCR prime
39	12.6	60.0	26	12	ADQ59923	ADQ59923 Probe mus
C 40	12.6	60.0	29	14	ADV67359	ADV67359 Primer fo
41	12.4	59.0	20	12	ADP81789	ADP81789 Human MD-
42	12.4	59.0	21	13	AEA91007	AEA91007 Human lup
43	12.4	59.0	25	9	ACI65108	ACI65108 Human mic
C 44	12.4	59.0	25	9	ACK17123	ACK17123 Human mic
45	12.2	58.1	19	6	AAI40885	AAI40885 Gamma toc

ALIGNMENTS

RESULT 1	ADRI6250 standard; RNA; 21 BP.
ID	ADRI6250
XX	XX
AC	ADRI6250;
XX	XX
DT	04-NOV-2004 (first entry)
XX	XX
DE	Human Pablo cDNA small interfering RNA (siRNA) molecule #1.
XX	XX
KW	-Pablo; sg; small interfering RNA; siRNA; apoptosis;
KW	Bcl-XL binding domain; nervous system disorder; neural cell; cell death;
KW	Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW	spinal muscular atrophy; cancer; neuroprotective; nootropic;
KW	antiparkinsonian; muscular; cyostatic.
XX	XX
OS	Synthetic.
XX	XX
PN	US2004157327-A1.
XX	XX
PD	12-AUG-2004.
XX	XX
PF	23-JUN-2003; 2003US-00601492.
XX	XX
PR	22-OCT-1999; 99US-00425501.
PR	15-MAY-2001; 2001US-00658155.
XX	XX
PA	(AMHP) WYETH.
XX	XX
PI	Mark RJ, Young KH, Wood AT;
XX	XX
DR	WPI; 2004-580273/56.
XX	XX
PT	New Pablo polypeptides and encoding nucleic acid molecules useful for
PT	modulating apoptosis (i.e. in neural cells), or for diagnosing,
PT	preventing or treating disorders associated with cell death, e.g.
XX	Alzheimer's disease or cancer.
XX	XX
PS	Claim 3; SEQ ID NO 3; 64pp; English.
XX	XX
CC	The invention relates to a small interfering RNA (siRNA) molecule that
CC	inhibits the expression of a Pablo polypeptide in a eukaryotic cell. The

CC invention also relates to a method for inhibiting apoptosis in a
CC mammalian cell, comprising administering the siRNA molecule to the cell,
CC a polypeptide comprising an isolated mammalian Bcl-XL binding domain, a
CC method of treating a nervous system disorder in a subject, a method of
CC detecting the presence of Pablo in a cell and a method of identifying a
CC compound that modulates the pro-apoptotic activity of a Bcl-XL binding
CC domain. The composition and methods are useful for modulating apoptosis,
CC particularly in neural cells, as well as for the diagnosis, treatment or
CC prevention of disorders that can benefit from modulation of cell death,
CC e.g. Alzheimer's disease, Parkinson's disease, amyotrophic lateral
CC sclerosis, spinal muscular atrophy and cancer. These may also be used in
CC drug screening assays or in pharmacogenomics. This sequence represents a
CC small interfering RNA (siRNA) molecule used to inhibit expression of
CC human Pablo CDNA of the invention.

XX Sequence 21 BP; 2 A; 4 C; 6 G; 0 T; 9 U; 0 Other;

Query Match 100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.54; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUGUGACCGUUUACUGU 21
|||
DB 1 CGUGUGACCGUUUACUGU 21

RESULT 2

ADRI6251/c
ID ADRI6251 standard; RNA; 21 BP.

AC ADRI6251;

DT 04-NOV-2004 (first entry)

XX Human Pablo CDNA small interfering RNA (siRNA) molecule #2.

DE Pablo; sg: small interfering RNA; siRNA; apoptosis;

KM Bcl-XL binding domain; nervous system disorder; neural cell; cell death;

KM Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;

KM spinal muscular atrophy; cancer; neuroprotective; neurotropic;

KM antiparkinsonian; muscular; cyostatic.

OS Synthetic.

PN US2004157327-A1.

XX 12-AUG-2004.

PD 23-JUN-2003; 2003US-00601492.

XX 22-OCT-1999; 99US-00425501.

PR 15-MAY-2001; 2001US-00858155.

XX (AMHP) WYETH.

PA Mark RJ, Young KH, Wood AT;

PI WPI; 2004-580273/56.

DR New Pablo polypeptides and encoding nucleic acid molecules useful for

XX PT modulating apoptosis (i.e. in neural cells), or for diagnosing,

PT PT preventing or treating disorders associated with cell death, e.g.

XX PT Alzheimer's disease or cancer.

XX Claim 3; SEQ ID NO 4; 64pp; English.

XX The invention relates to a small interfering RNA (siRNA) molecule that

CC inhibits the expression of a Pablo polypeptide in a eukaryotic cell. The

CC invention also relates to a method for inhibiting apoptosis in a

CC mammalian cell, comprising administering the siRNA molecule to the cell,

CC a polypeptide comprising an isolated mammalian Bcl-XL binding domain, a

CC method of treating a nervous system disorder in a subject, a method of

CC detecting the presence of Pablo in a cell and a method of identifying a

CC compound that modulates the pro-apoptotic activity of a Bcl-XL binding
CC domain. The composition and methods are useful for modulating apoptosis,
CC particularly in neural cells, as well as for the diagnosis, treatment or
CC prevention of disorders that can benefit from modulation of cell death,
CC e.g. Alzheimer's disease, Parkinson's disease, amyotrophic lateral
CC sclerosis, spinal muscular atrophy and cancer. These may also be used in
CC drug screening assays or in pharmacogenomics. This sequence represents a
CC small interfering RNA (siRNA) molecule used to inhibit expression of
CC human Pablo CDNA of the invention.

XX Sequence 21 BP; 7 A; 6 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 90.5%; Score 19; DB 13; Length 21;
Best Local Similarity 63.2%; Pred. No. 5.9;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUGUGACCGUUUACUG 19
|||
DB 19 CGUGUGACCGUUUACUG 1

RESULT 3

ACII17033
ID ACII17033 standard; DNA; 25 BP.

XX ACII17033;

DT 13-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 17024.

DE EST; sg: probe; expressed sequence tag; microarray; gene expression;

KM genetic variation; diallelic marker; polymorphism; human;

KM cross-species comparison.

OS Homo sapiens.

PN US2003104410-A1.

XX 05-JUN-2003.

PF 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFY-) AFFIMETRIX INC.

XX Miltmann MP;

XX WPI; 2003-567953/53.

DR New array of nucleic acid probes, useful for in situ hybridization, in

XX PT Southern, Northern or dot-blot hybridization to identify or detect the

XX PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 17024; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic

XX acid probes including one of 2,018,500 fully defined sequences, or its

XX perfect match, perfect mismatch, antisense match or antisense mismatch.

XX Also disclosed is a method of gene expression analysis. The array is used

XX in monitoring gene expression levels by hybridisation to a DNA library,

XX in analysis of genetic variation or in hybridisation of tag-labelled

XX compounds. The nucleic acid probes are specifically designed for analysis

XX of at least one target sequence. The method of analysis comprises

XX hybridising at least one or more nucleic acids to at least two or more

XX nucleic acid probes and detecting the hybridisation. The nucleic acid

XX probes are attached to a solid support. The analysis comprises monitoring

XX gene expression levels, identifying diallelic markers or polymorphisms,

XX or family members of a gene and a cross-species comparison. Each of the

XX nucleic acids further comprises a tag sequence. The array of nucleic acid

XX probes is useful in in situ hybridisation, in Southern, Northern or dot-

XX blot hybridisation to identify or detect the sequence or specific